

FIGURE 1

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Eciss  ATGCAGGATAATAAGATGAAAAAATGTTATTTCTGCCGCTCTGGCAATGCTTATTACA  60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
102iss ATGCAGGATAATAAGATGAAAAAATGTTATTTCTGCCGCTCTGGCAATGCTTATTACA  60
      ||||| | |||||||||||| | | | | | | | | |||||||||||
lambor ATCGGGAATAACACCATGAAAAAATGCTACTCGCTACTGCGCTGGCCCTGCTTATTACA  60

Eciss  GGATGTGCTCAACAAACGTTTACTGTTGGAAACAAACCGACAGCAGTAACA/CANAGGAA  120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
102iss GGATGTGCTCAACAAACGTTTACTGTTGGAAACAAACCGACAGCAGTAACACCAAAGGAA  120
      |||||||||||||||| | |||||||||| | |||||||| | |||||||| |
lambor GGATGTGCTCAACAGACGTTTACTGTTCAAAACAAACCGGCAGCAGTAGCACCAAAGGAA  120

Eciss  ACCATCACTCATCATTTCTTCGTTTCCCCAATTGGAC-AGAGAAAACGTGTGATGCAGCC  179
      ||||||| | ||||||| | ||||||| | ||||||| | ||||||| |
102iss ACCATCACTCATCATTTCTTCGTTTCCGGAATTGGACAAGAGAAAACGTGTGATGCAGCC  180
      ||||||| | ||||||| | ||||||| | ||||||| | ||||||| |
lambor ACCATCACCCATCATTTCTTCGTTTCTGGAATTGGGCAGAAGAAAACGTGCGATGCAGCC  180

Eciss  AAAATTTGTTGGCGGTGCAGAAAATGTTGTTAAACAGAAACTCAGCAAACATTTCGTAAA  239
      ||||||| | ||||||| | ||||||| | ||||||| | ||||||| |
102iss AAAATTTG-TGGCGGTGCAGAAAATGTTGTTAAACAGAAACTCAGCAAACATTTCGTAAA  239
      ||||||| | ||||||| | ||||||| | ||||||| | ||||||| |
lambor AAAATTTG-TGGCGGCGCAGAAAATGTTGTTAAACAGAAACCCAGCAAACATTTCGTAAA  239

Eciss  TGCATTGCCCGGTTTTATCACTTTTGGCATCTATACTCCGCGGGAAACCCGTGTATATTG  299
      || ||||| | ||||||| | ||||||| | ||||||| | ||||||| |
102iss TGGATTGCTCGGTTTTATCACTTTTGGCATCTATACTCCGCTGGAAGCCCGGGTATATTG  299
      ||||||| | ||||||| | ||||||| | ||||||| | ||||||| |
lambor TGGATTGCTCGGTTTTATTACTTTAGGCATTTATACTCCGCTGGAAGCGCGTGTATTG  299

Eciss  CTCACAATAG  309
      |||||||||
102iss CTCACAATAG  309
      |||||||||
lambor CTCACAATAA  309
  
```

FIGURE 2

Iss_Ec	MQDNKMKKMLFSAALAMLITGCAQQTFTVGNKPTAVTPKETITHHFFVSPIGQRKLLMQP	60
	:	
102Iss	MQDNKMKKMLFSAALAMLITGCAQQTFTVGNKPTAVTPKETITHHFFVSGIGQEKTVDA	60
	:	
lamBor	MKKMLLATALALLITGCAQQTFTVQNKPAAVAPKETITHHFFVSGIGQKKTVDAA	55
Iss_Ec	KFVGGAENVVKTETQQTFFVNALPGFITFGIYTPRETRVYCSQ	102
	: :	
102Iss	KICGGAENVVKTETQQTFFVNGLLGFITFGIYTPLEARVYCSQ	102
	:	
lamBor	KICGGAENVVKTETQQTFFVNGLLGFITLGIYTPLEARVYCSQ	97

FIGURE 3

L E V L F Q G P L G S M Q D N
CTG GAA GTT CTG TTC CAG GGG CCC CTG GGA TCC ATG CAG GAT AAT
PreScission Protease BamHI iss fusion start

K M K K M L F S A A L A M L I
AAG ATG AAA AAA ATG TTA TTT TCT GCC GCT CTG GCA ATG CTT ATT

T G C A Q Q T F T V G N K P T
ACA GGA TGT GCT CAA CAA ACG TTT ACT GTT GGA AAC AAA CCG ACA

A V T P K E T I T H H F F V S
GCA GTA ACA CCA AAG GAA ACC ATC ACT CAT CAT TTC TTC GTT TCG

G I G Q E K T V D A A K I C G
GGA ATT GGA CAA GAG AAA ACT GTT GAT GCA GCC AAA ATT TGT GGC

G A E N V V K T E T Q Q T F V
GGT GCA GAA AAT GTT GTT AAA ACA GAA ACT CAG CAA ACA TTC GTA

N G L L G F I T F G I Y T P L
AAT GGA TTG CTC GGT TTT ATC ACT TTT GGC ATC TAT ACT CCG CTG

E A R V Y C S Q *
GAA GCC CGG GTA TAT TGC TCA CAA TAG TTG CCC ATC GAT ATG GGG

AGC TCA TCT GCG AAT TCC
EcoRI

FIGURE 4

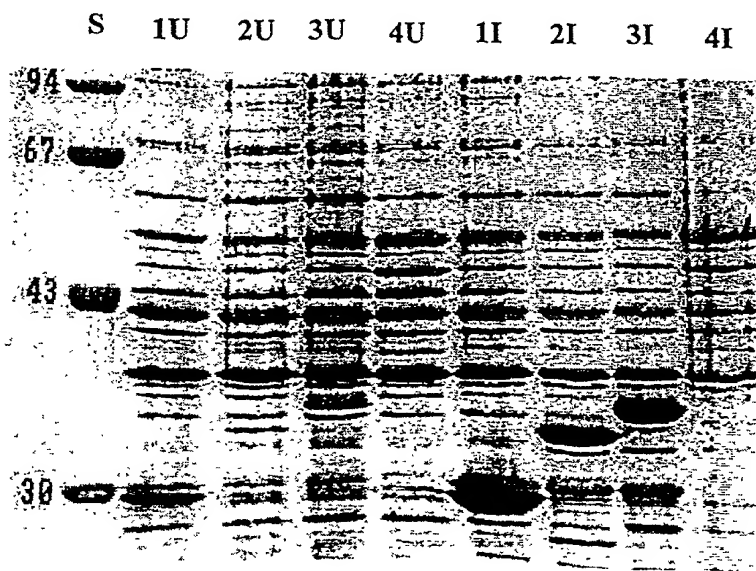
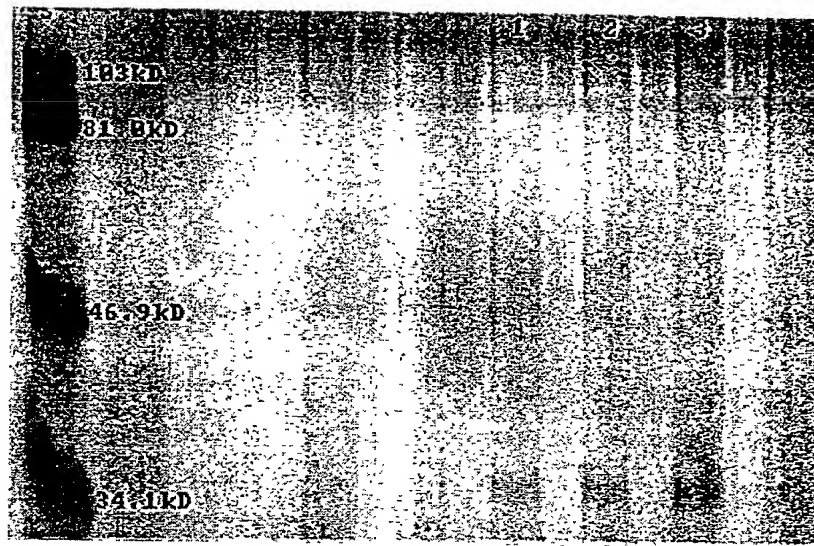


FIGURE 5



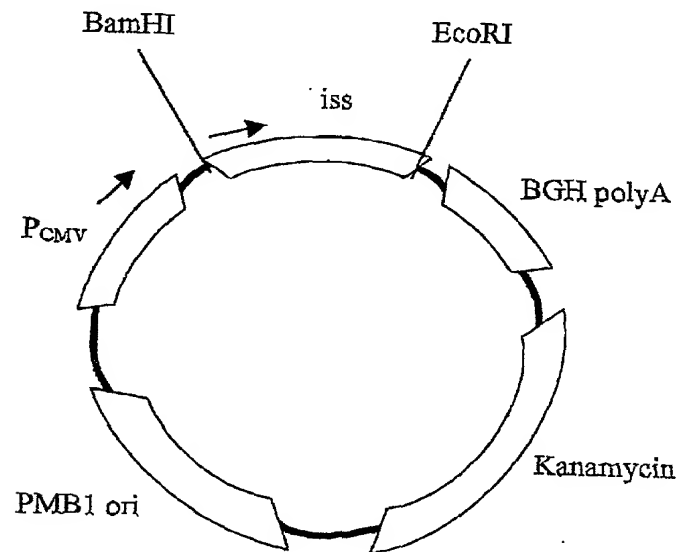


Fig 6